| 54 GGC | 108 AGT S | 162 GGC G | 216 CAT H | 270 CGG R | 324 CCT P |
|---------------|----------------------|-----------------|------------------|-----------------|-----------------|
| CGC | TTC | TAT Y | CCC | TGT | TTT F |
| AGC | ACC S | GAT D | ATC I | GCC | GGA G |
| 45 AGC | 99 TTA | 153 GAG E | 207 CCC P | 261 AGT S | 315 TTT F |
| GGA | GCA A | TTA L | TCC | AGT | GCC |
| 36 GAA GCS | 90 CTC GTG L V | GCC | ATC I | ACC | TCT |
| 36 GAA | 90 CTC L | 144 TGT C | 198 GGC ATC ' | 252 GCA A | 306 GTT V |
| CAG | GCT | GGA | CAC H | GAT D | GTT V |
| TGG | AAA K | CTG | TTC | TCA S | ATT I |
| 27 CCG | 81 GTT V | 135 ATG M | 189 ATT I | 243 GAC D | 297 GGA . |
| 999 | 9 9 | CTT L | GTC.CTG V L | TAT Y | ACT |
| CCC | GCG | TTT F | GTC | ACC | ACT |
| 18 CTG | 72 ATG M | 126 ACT T | 180 TTC F | 234 GTC V | 288 TTC F |
| AGG | GAC | CTG | TTA L | AGA R | TTC |
| 299 | GGA | GGA G | CCC | AAA K | 279 GCA TAT |
| 9 TTG | 63 TCG | 117 ATT I | 171 TGG W | 225 GCC A | 279 GCA A |
| TCT GGC | CCC AGT | GGG GCT G A | GTT TAC V Y | ATT I | CTG |
| | 222 | 999 9 | GTT V | TTC F | GAA CTG E L |
| <u>.</u> | | | | | /: |

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| 378 TTG L | 432 GGA G | 486 GTG | 540 TTT | 594 CAC | 648 CCT |
|-----------------|---------------------|-----------------|------------|------------|------------|
| GTG V | TTT F | ACA | GCA | GTT | AGA |
| CTT | ATA I | ATT | 929 | CAT | AAT |
| 369 GGC G | 423 CTT L | 477 CTG | 531 CAT | 585 TAT | 639 GCA |
| TGC C | TTC | ATT | GCA | ATA | TCA |
| GCC A | TTT F | TTT | TGT | TTT | TTC |
| 360 GGA G | 414 GGG | 468 CAC | 522 ACA | 576 ACC | 630 TTA |
| TGG M | CAA Q | TAG | TAT | AAT | GTT |
| AAA K | ATT I | TGG W | CTG | TTT | TGA |
| 351 ATC I | 405 ACA T | 459 CAG Q | 513 TAT | 567 TTT | 621 AGA |
| GTG V | CTT | GAG E | TAC | 999 | AGG |
| GCT A | TTC | TGG W | TCA | GCT | AGT |
| 342 GTG V | 396 ATT I | 450 AGC S | 504 AAC | 558 TAT | 612 ATA |
| CGT R | GTC V | TTT | TAG | TAA | TTC |
| GCT | GCA A | GAT D | TCT | ATT | GAC |
| 333 CTT L | 387 C AAT 0 N | 441 GAT D | 495 ATT | 549 Gaa | 603 AAA |
| ATT I | 9 9 | GGA | CAT TGA | TAT | AAG |
| GTT V | GCA GGC A G | AGA GGA R G | CAT | TAC | TTT |

FIGURE 1B

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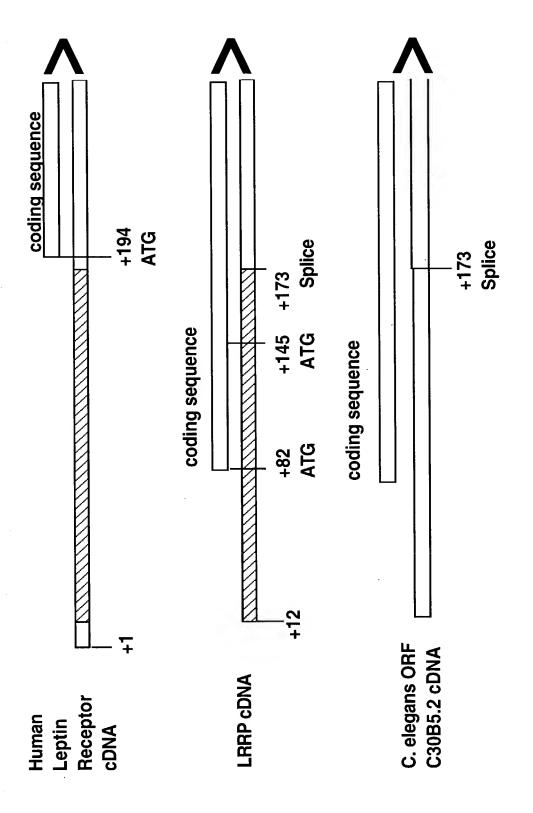
| 702 GTA | 756 CCT | 810 AAC | 864 TTT |
|------------|------------|------------|-------------|
| CAT | CCA | GAT | TTK |
| GTT | CTG | GCA | T CT |
| 693 GCT | 747 CAG | 801 GAG | 855 CCC |
| TTG | AGG | GGA | GWT |
| TGT | TGT | CTT | GTG |
| 684 ACT | 738 TCT | 792 GTG | 846 GGG |
| GTT | CAG | GAT | O C C |
| TAT | ACG | 999 | AAG |
| 675 AAT | 729 TTA | 783 CTT | 837 AGG |
| TCA | ATA | TTG | 222 |
| TAC | AAT | CTT | TGA |
| 666 TGT | 720 GAA | 774 AAC | 828 TCA |
| TTA | TCA | CGA | CTC |
| AGA | CTC | CAT | 9 0 |
| 657 TTT | 711 GTG | 765 GTG | 819 GCA |
| GTC AAA | ACG | GCA | GAA |
| GTC | GTC | TAT | GCT |

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The Electronic Northern for Clone: 492703 and Stringency >=50

| Library | Lib Description | Abun | Pct Abun |
|-----------|--|----------------|-----------------|
| | | 1 1 1 1 | 1 1 1 1 1 1 1 1 |
| RATRNOT01 | heart, right atrium, 51 F | \leftarrow I | 0.0861 |
| SYNORAB01 | synovium, hip, rheumatoid, 68 F | 4 | 0.0779 |
| LIVRNOM01 | liver, 49 M, WM | \vdash | 0.0254 |
| PLACNOB01 | placenta, neonatal F | | 0.0225 |
| BRSTNOT01 | breast, 56 F | \leftarrow | 0.0192 |
| HNT2AGT01 | hNT-2 cell line, post-mitotic neurons | \vdash | 0.0190 |
| HNT2NOT01 | hNT-2 cell line, teratocarcinoma, control | \vdash | 0.0172 |
| BRSTTUT03 | breast tumor, 58 F, match to BRSTNOT05 | \leftarrow | 0.0148 |
| COLNFET02 | colon, fetal F | \leftarrow | 0.0142 |
| UCMCL5T01 | lymphocytes (umbilical cord), treated IL-5 | \leftarrow I | 0.0125 |
| MELANOM01 | melanocytes, M, NORM, WM | \vdash | 0.0108 |
| PLACNOM02 | placenta, neonatal F, NORM, WM | \vdash | 0.0056 |

FIGURE 2

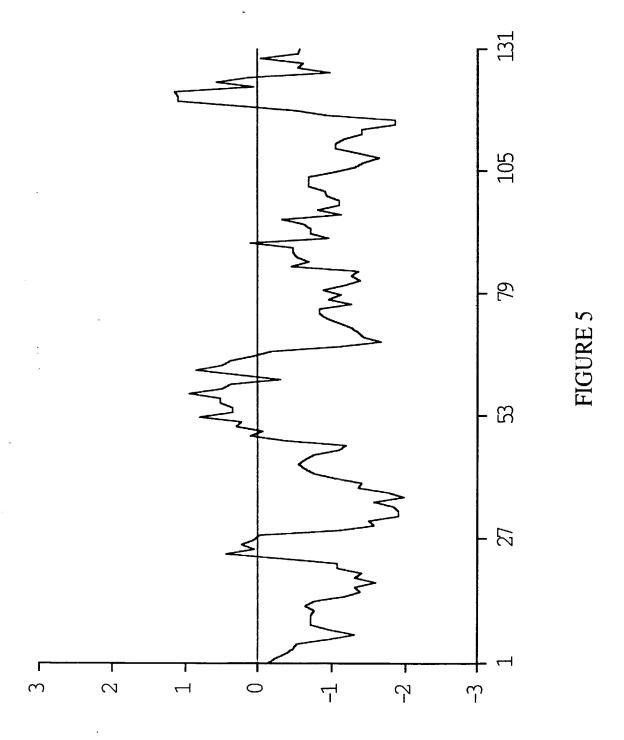


Numbering relative to human leptin receptor
 Hatched area represents identical sequences

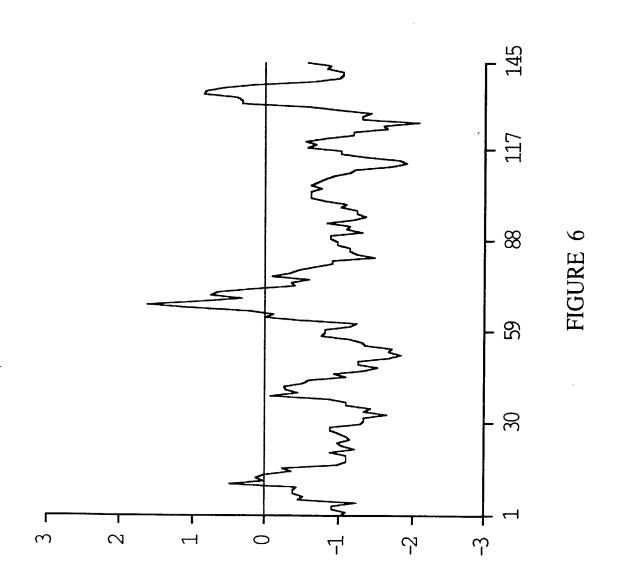
FIGURE 3

| FIM L SEQ ID NO-1 | YDSDSEQIDNO-1 | AVIKWGA SEQ ID NO-1 | SEQ ID NO-1 |
|------------------------------------|---------------------------------------|-------------------------------------|--|
| FLV L SEQ ID NO-3 | FQEDSEQIDNO-3 | GTIAMSA SEQ ID NO-3 | SEQ ID NO-3 |
| FLVIL SEQ ID NO-4 | YHTSDFSEQIDNO-4 | QLIGHLS SEQ ID NO-4 | SEQ ID NO-4 |
| M AGVKALVALSFSGAIGLT | 4 GCALEDYGVYWPLFVLIFHGISPIPHFIAKRVT-9 | - ATSS-ACRELAYFFTTGIVVSAFGFPVILARVA | 99 CGIVLAGNAVIFLTIQGFFLIFGRGDDFSWEQW |
| MCCHIHIQCFDCCSMKNTILAVAALAEAGVVGLT | GCALPRYGTWTPMFVITEYVLSPVPLLIARR | - MTGTNACIELALFITTGIVISAFALPIVLAHA | 113 CFLIFIANSINFSVIIFYERIFNGEDMNGMSLW |
| M MEFKVSPLTKII SLSGFLALG | SCALFHNYYPLFDILIFLAPIPNTIFNAGNK | MSDSSNTGQDLAHFLTGMLVTSGIALPVVFYHC | 107 CIMCMIGGLIIYSSIVIEKWFEKKDFNEDDSLFG |
| \leftarrow | % % % | 67 74 67 | 8, 11, 14 |

FIGURE 4



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Human genomic organization of OB-RGRP

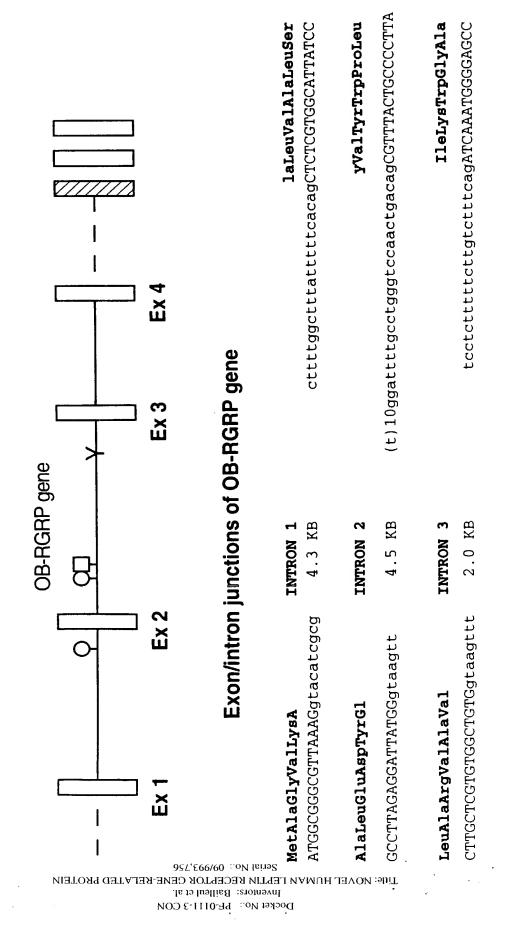
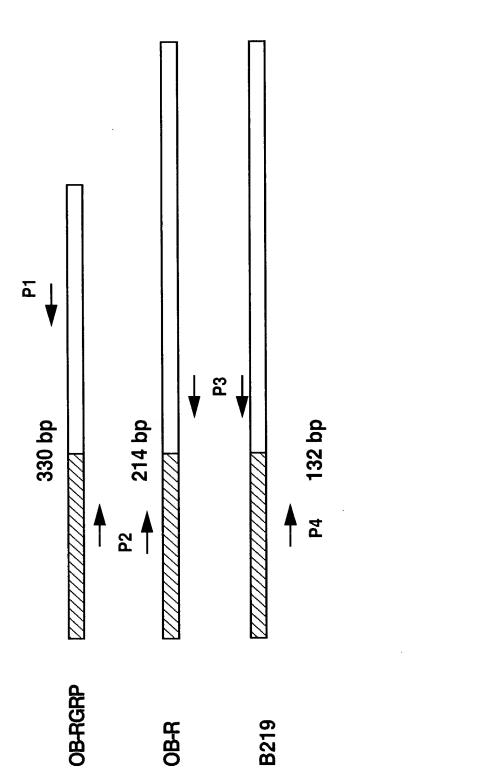


FIGURE 7

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Marker
HSBS
HUGO
HUGO
HUGO
HUGO
HUGO
HUGO

.q ibA

FIGURE 9

330 bp 330 bp 28-R 214 bp 8219